

SEQUENCE LISTING

<110> Glotzer, Michael  
Jantsch-Plunger, Verena  
Romano, Alper  
Mishima, Masanori  
Kaitna, Susanne

<120> Cyk-4 polypeptides, DNA molecules encoding them and their use in screening methods

<130> 0652.2260001/EKS/AES

<140>

<141>

<150> EP 00 112 880.0  
<151> 2000-06-19

<150> EP 01 110 554.1  
<151> 2001-04-30

<150> 60/241,231  
<151> 2000-10-18

<150> To be determined  
<151> 2001-06-13

<160> 6

<170> PatentIn Ver. 2.1

<210> 1  
<211> 3050  
<212> DNA  
<213> Homo sapiens

<220>  
<221> 5'UTR  
<222> (1)..(70)

<220>  
<221> CDS  
<222> (71)..(1969)

<220>  
<221> 3'UTR  
<222> (1970)..(3050)

<400> 1

taaagggggg tgccagacca ggtgcgtctg ccgctggatt gtgataggaa gcagagtgtt 60  
cgtgtgaaag atg gat act atg ctg aat gtg cgg aat ctg ttt gag 109  
Met Asp Thr Met Met Leu Asn Val Arg Asn Leu Phe Glu  
1 5 10  
cag ctt gtg cgc cgg gtg gag att ctc agt gaa gga aat gaa gtc caa 157  
Gln Leu Val Arg Arg Val Glu Ile Leu Ser Glu Gly Asn Glu Val Gln  
15 20 25  
ttt atc cag ttg gcg aag gac ttt gag gat ttc cgt aaa aag tgg cag 205  
Phe Ile Gln Leu Ala Lys Asp Phe Glu Asp Phe Arg Lys Lys Trp Gln  
30 35 40 45  
agg act gac cat gag ctg ggg aaa tac aag gat ctt ttg atg aaa gca 253  
Arg Thr Asp His Glu Leu Gly Lys Tyr Lys Asp Leu Leu Met Lys Ala  
50 55 60  
gag act gag cga agt gct ctg gat gtt aag ctg aag cat gca cgt aat 301  
Glu Thr Glu Arg Ser Ala Leu Asp Val Lys Leu Lys His Ala Arg Asn  
65 70 75  
cag gtg gat gta gag atc aaa cgg aga cag aga gct gag gct gac tgc 349  
Gln Val Asp Val Glu Ile Lys Arg Arg Gln Arg Ala Glu Ala Asp Cys  
80 85 90  
gaa aag ctg gaa cga cag att cag ctg att cga gag atg ctc atg tgt 397  
Glu Lys Leu Glu Arg Gln Ile Gln Leu Ile Arg Glu Met Leu Met Cys  
95 100 105  
gac aca tct ggc agc att caa cta agc gag gag caa aaa tca gct ctg 445  
Asp Thr Ser Gly Ser Ile Gln Leu Ser Glu Glu Gln Lys Ser Ala Leu  
110 115 120 125  
gct ttt ctc aac aga ggc caa cca tcc agc agc aat gct ggg aac aaa 493  
Ala Phe Leu Asn Arg Gly Gln Pro Ser Ser Ser Asn Ala Gly Asn Lys  
130 135 140  
aga cta tca acc att gat gaa tct ggt tcc att tta tca gat atc agc 541  
Arg Leu Ser Thr Ile Asp Glu Ser Gly Ser Ile Leu Ser Asp Ile Ser  
145 150 155  
ttt gac aag act gat gaa tca ctg gat tgg gac tct tct ttg gtg aag 589  
Phe Asp Lys Thr Asp Glu Ser Leu Asp Trp Asp Ser Ser Leu Val Lys

	160	165	170	
act ttc aaa ctg aag aag aga gaa aag agg cgc tct act agc cga cag				637
Thr Phe Lys Leu Lys Lys Arg Glu Lys Arg Arg Ser Thr Ser Arg Gln				
175	180	185		
ttt gtt gat ggt ccc cct gga cct gta aag aaa act cgt tcc att ggc				685
Phe Val Asp Gly Pro Pro Gly Pro Val Lys Lys Thr Arg Ser Ile Gly				
190	195	200		205
tct gca gta gac cag ggg aat gaa tcc ata gtt gca aaa act aca gtg				733
Ser Ala Val Asp Gln Gly Asn Glu Ser Ile Val Ala Lys Thr Thr Val				
210	215	220		
act gtt ccc aat gat ggc ggg ccc atc gaa gct gtg tcc act att gag				781
Thr Val Pro Asn Asp Gly Gly Pro Ile Glu Ala Val Ser Thr Ile Glu				
225	230	235		
act gtg cca tat tgg acc agg agc cga agg aaa aca ggt act tta caa				829
Thr Val Pro Tyr Trp Thr Arg Ser Arg Arg Lys Thr Gly Thr Leu Gln				
240	245	250		
cct tgg aac agt gac tcc acc ctg aac agc agg cag ctg gag cca aga				877
Pro Trp Asn Ser Asp Ser Thr Leu Asn Ser Arg Gln Leu Glu Pro Arg				
255	260	265		
act gag aca gac agt gtg ggc acg cca cag agt aat gga ggg atg cgc				925
Thr Glu Thr Asp Ser Val Gly Thr Pro Gln Ser Asn Gly Gly Met Arg				
270	275	280		285
ctg cat gac ttt gtt tct aag acg gtt att aaa cct gaa tcc tgt gtt				973
Leu His Asp Phe Val Ser Lys Thr Val Ile Lys Pro Glu Ser Cys Val				
290	295	300		
cca tgt gga aag cgg ata aaa ttt ggc aaa tta tct ctg aag tgt cga				1021
Pro Cys Gly Lys Arg Ile Lys Phe Gly Lys Leu Ser Leu Lys Cys Arg				
305	310	315		
gac tgt cgt gtg gtc tct cat cca gaa tgt cgg gac cgc tgt ccc ctt				1069
Asp Cys Arg Val Val Ser His Pro Glu Cys Arg Asp Arg Cys Pro Leu				
320	325	330		
ccc tgc att cct acc ctg ata gga aca cct gtc aag att gga gag gga				1117
Pro Cys Ile Pro Thr Leu Ile Gly Thr Pro Val Lys Ile Gly Glu Gly				
335	340	345		

atg ctg gca gac ttt gtg tcc cag act tct cca atg atc ccc tcc att 1165  
Met Leu Ala Asp Phe Val Ser Gln Thr Ser Pro Met Ile Pro Ser Ile  
350 355 360 365  
gtt gtg cat tgt gta aat gag att gag caa aga ggt ctg act gag aca 1213  
Val Val His Cys Val Asn Glu Ile Glu Gln Arg Gly Leu Thr Glu Thr  
370 375 380  
ggc ctg tat agg atc tct ggc tgt gac cgc aca gta aaa gag ctg aaa 1261  
Gly Leu Tyr Arg Ile Ser Gly Cys Asp Arg Thr Val Lys Glu Leu Lys  
385 390 395  
gag aaa ttc ctc aga gtg aaa act gta ccc ctc ctc agc aaa gtg gat 1309  
Glu Lys Phe Leu Arg Val Lys Thr Val Pro Leu Leu Ser Lys Val Asp  
400 405 410  
gat atc cat gct atc tgt agc ctt cta aaa gac ttt ctt cga aac ctc 1357  
Asp Ile His Ala Ile Cys Ser Leu Leu Lys Asp Phe Leu Arg Asn Leu  
415 420 425  
aaa gaa cct ctt ctg acc ttt cgc ctt aac aga gcc ttt atg gaa gca 1405  
Lys Glu Pro Leu Leu Thr Phe Arg Leu Asn Arg Ala Phe Met Glu Ala  
430 435 440 445  
gca gaa atc aca gat gaa gac aac agc ata gct gcc atg tac caa gct 1453  
Ala Glu Ile Thr Asp Glu Asp Asn Ser Ile Ala Ala Met Tyr Gln Ala  
450 455 460  
gtt ggt gaa ctg ccc cag gcc aac agg gac aca tta gct ttc ctc atg 1501  
Val Gly Glu Leu Pro Gln Ala Asn Arg Asp Thr Leu Ala Phe Leu Met  
465 470 475  
att cac ttg cag aga gtg gct cag agt cca cat act aaa atg gat gtt 1549  
Ile His Leu Gln Arg Val Ala Gln Ser Pro His Thr Lys Met Asp Val  
480 485 490  
gcc aat ctg gct aaa gtc ttt ggc cct aca ata gtg gcc cat gct gtg 1597  
Ala Asn Leu Ala Lys Val Phe Gly Pro Thr Ile Val Ala His Ala Val  
495 500 505  
ccc aat cca gac cca gtg aca atg tca cag gac atc aag cgt caa ccc 1645  
Pro Asn Pro Asp Pro Val Thr Met Ser Gln Asp Ile Lys Arg Gln Pro  
510 515 520 525

aag gtg gtt gag cgc ctg ctt tcc ttg cct ctg gag tat tgg agt cag 1693  
Lys Val Val Glu Arg Leu Leu Ser Leu Pro Leu Glu Tyr Trp Ser Gln  
530 535 540

ttc atg atg gtg gag caa gag aac att gac ccc cta cat gtc att gaa 1741  
Phe Met Met Val Glu Gln Glu Asn Ile Asp Pro Leu His Val Ile Glu  
545 550 555

aac tca aat gcc ttt tca aca cca cag aca cca gat att aaa gtg agt 1789  
Asn Ser Asn Ala Phe Ser Thr Pro Gln Thr Pro Asp Ile Lys Val Ser  
560 565 570

tta ctg gga cct gtg acc act cct gaa cat cag ctt ctc aag act cct 1837  
Leu Leu Gly Pro Val Thr Thr Pro Glu His Gln Leu Leu Lys Thr Pro  
575 580 585

tca tct agt tcc ctg tca cag aga gtc cgt tcc acc ctc acc aag aac 1885  
Ser Ser Ser Ser Leu Ser Gln Arg Val Arg Ser Thr Leu Thr Lys Asn  
590 595 600 605

act cct aga ttt ggg agc aaa agc aag tct gcc act aac cta gga cga 1933  
Thr Pro Arg Phe Gly Ser Lys Ser Ala Thr Asn Leu Gly Arg  
610 615 620

caa ggc aac ttt ttt gct tct cca atg ctc aag tga agtcacatct 1979  
Gln Gly Asn Phe Phe Ala Ser Pro Met Leu Lys  
625 630

gcctgttact tccccaggatt gactgactat aagaaaggac acatctgtac tctgtctgc 2039

agcctcctgt actcattact acttttagca ttctccaggc ttttactcaa gttaattgt 2099

gcatgagggt tttattaaaa ctatataatat ctcccccttcc ttctcctcaa gtcacataat 2159

atcagcactt tttgtgtggc attgttggga gtttttagat gagacatctt tccagggtta 2219

gaagggttag tatggaaattt gttgtgattt tttttggga agggggttat tttttttttt 2279

gcttaaagcc aatgtgtgtt catagaatga tctttctcta gtttcatatata gaaactgtttt 2339

ccgtgagaca atgacagaaa ccctacctat ctgataagat tagcttgc tttttttttt 2399

agtgggaggg cagggcaaag aaaggattag accagagat ttaggatgcc tccttctaag 2459  
aaccagaagt ttcattccc cattatgaac tgagctataa tatggagctt tcataaaaat 2519  
gggatgcatt gaggacagaa ctatgtatgg gatgtatgcgt agcttgatt tggatgatta 2579  
ggcttttaat agtgttgagt ggcacaaccc tggaaatgtg aaagtacaac tcgtatTTT 2639  
ctctgatgtg ccgctggctg aactttgggt tcatttgggg tcaaagccag tttttcttt 2699  
aaaattgaat tcattctgat gcttggcccc cataccccc accttgcaca gtggagccca 2759  
acttctaaag gtcaatataat catcctttgg catcccaact accaataaag agtaggctat 2819  
aagggaaagat tgtcaatatt ttgtggtaag aaaagctaca gtcattttt ctttgcactt 2879  
tggatgctga aatttttccc atggaacata gccacatcta gatagatgtg agtttttct 2939  
tctgttaaaa ttatcttaa tgtctgtaaa aacgattttc ttctgttagaa tggggactt 2999  
cgtattgacc cttatctgta aaacacctat ttgggataat atttggcttt a 3050

<210> 2  
<211> 632  
<212> PRT  
<213> Homo sapiens

<400> 2

Met Asp Thr Met Met Leu Asn Val Arg Asn Leu Phe Glu Gln Leu Val  
1 5 10 15

Arg Arg Val Glu Ile Leu Ser Glu Gly Asn Glu Val Gln Phe Ile Gln  
20 25 30

Ile Ala Lys Asp Phe Glu Asp Phe Arg Lys Lys Trp Gln Arg Thr Asp  
35 40 45

His Glu Leu Gly Lys Tyr Lys Asp Leu Leu Met Lys Ala Glu Thr Glu  
50 55 60

Arg Ser Ala Leu Asp Val Lys Leu Lys His Ala Arg Asn Gln Val Asp  
65 70 75 80

Val Glu Ile Lys Arg Arg Gln Arg Ala Glu Ala Asp Cys Glu Lys Leu  
85 90 95

Glu Arg Gln Ile Gln Leu Ile Arg Glu Met Leu Met Cys Asp Thr Ser  
100 105 110

Gly Ser Ile Gln Leu Ser Glu Glu Gln Lys Ser Ala Leu Ala Phe Leu  
115 120 125

Asn Arg Gly Gln Pro Ser Ser Ser Asn Ala Gly Asn Lys Arg Leu Ser  
130 135 140

Thr Ile Asp Glu Ser Gly Ser Ile Leu Ser Asp Ile Ser Phe Asp Lys  
145 150 155 160

Thr Asp Glu Ser Leu Asp Trp Asp Ser Ser Leu Val Lys Thr Phe Lys  
165 170 175

Leu Lys Lys Arg Glu Lys Arg Arg Ser Thr Ser Arg Gln Phe Val Asp  
180 185 190

Gly Pro Pro Gly Pro Val Lys Lys Thr Arg Ser Ile Gly Ser Ala Val  
195 200 205

Asp Gln Gly Asn Glu Ser Ile Val Ala Lys Thr Thr Val Thr Val Pro  
210 215 220

Asn Asp Gly Gly Pro Ile Glu Ala Val Ser Thr Ile Glu Thr Val Pro  
225 230 235 240

Tyr Trp Thr Arg Ser Arg Arg Lys Thr Gly Thr Leu Gln Pro Trp Asn  
245 250 255

Ser Asp Ser Thr Leu Asn Ser Arg Gln Leu Glu Pro Arg Thr Glu Thr  
260 265 270

Asp Ser Val Gly Thr Pro Gln Ser Asn Gly Gly Met Arg Leu His Asp  
275 280 285

Phe Val Ser Lys Thr Val Ile Lys Pro Glu Ser Cys Val Pro Cys Gly  
290 295 300

Lys Arg Ile Lys Phe Gly Lys Leu Ser Leu Lys Cys Arg Asp Cys Arg  
305 310 315 320

Val Val Ser His Pro Glu Cys Arg Asp Arg Cys Pro Leu Pro Cys Ile  
325 330 335

Pro Thr Leu Ile Gly Thr Pro Val Lys Ile Gly Glu Gly Met Leu Ala  
340 345 350

Asp Phe Val Ser Gln Thr Ser Pro Met Ile Pro Ser Ile Val Val His  
355 360 365

Cys Val Asn Glu Ile Glu Gln Arg Gly Leu Thr Glu Thr Gly Leu Tyr

370

375

380

Arg Ile Ser Gly Cys Asp Arg Thr Val Lys Glu Leu Lys Glu Lys Phe  
385 390 395 400

Leu Arg Val Lys Thr Val Pro Leu Leu Ser Lys Val Asp Asp Ile His  
405 410 415

Ala Ile Cys Ser Leu Leu Lys Asp Phe Leu Arg Asn Leu Lys Glu Pro  
420 425 430

Leu Leu Thr Phe Arg Leu Asn Arg Ala Phe Met Glu Ala Ala Glu Ile  
435 440 445

Thr Asp Glu Asp Asn Ser Ile Ala Ala Met Tyr Gln Ala Val Gly Glu  
450 455 460

Leu Pro Gln Ala Asn Arg Asp Thr Leu Ala Phe Leu Met Ile His Leu  
465 470 475 480

Gln Arg Val Ala Gln Ser Pro His Thr Lys Met Asp Val Ala Asn Leu  
485 490 495

Ala Lys Val Phe Gly Pro Thr Ile Val Ala His Ala Val Pro Asn Pro  
500 505 510

Asp Pro Val Thr Met Ser Gln Asp Ile Lys Arg Gln Pro Lys Val Val  
515 520 525

Glu Arg Leu Leu Ser Leu Pro Leu Glu Tyr Trp Ser Gln Phe Met Met  
530 535 540

Val Glu Gln Glu Asn Ile Asp Pro Leu His Val Ile Glu Asn Ser Asn  
545 550 555 560

Ala Phe Ser Thr Pro Gln Thr Pro Asp Ile Lys Val Ser Leu Leu Gly  
565 570 575

Pro Val Thr Thr Pro Glu His Gln Leu Leu Lys Thr Pro Ser Ser Ser  
580 585 590

Ser Leu Ser Gln Arg Val Arg Ser Thr Leu Thr Lys Asn Thr Pro Arg  
595 600 605

Phe Gly Ser Lys Ser Lys Ser Ala Thr Asn Leu Gly Arg Gln Gly Asn  
610 615 620

Phe Phe Ala Ser Pro Met Leu Lys  
625 630

<210> 3

<211> 2919

<212> DNA

<213> Mus musculus

<220>  
<221> 5'UTR  
<222> (1)..(134)

<220>  
<221> CDS  
<222> (135)..(2021)

<220>  
<221> 3'UTR  
<222> (2022)..(2919)

<400> 3

ggaaagcgggt tttacactgc cgtagtgag ggcgtcgct ggttagacagc agccctctg 60

gggcgcggcg gccggagagt gagcgcgcg ggccggacgg gttgcgtgt ggcggggcc 120

gggagcctcg aaag atg gat act aca atg gtg aat ttg tgg act ctg ttt 170

Met Asp Thr Thr Met Val Asn Leu Trp Thr Leu Phe  
1 5 10

gag cag ctt gtg cgc cgg atg gag att atc aat gaa gga aat gaa agc 218

Glu Gln Leu Val Arg Arg Met Glu Ile Ile Asn Glu Gly Asn Glu Ser  
15 20 25

att gaa ttc atc cag gtt gtg aag gac ttc gag gac ttc cga aag aag 266

Ile Glu Phe Ile Gln Val Val Lys Asp Phe Glu Asp Phe Arg Lys Lys  
30 35 40

tat caa aga acc aac cag gag ctg gag aaa ttc aaa gac cta ttg ttg 314

Tyr Gln Arg Thr Asn Gln Glu Leu Glu Lys Phe Lys Asp Leu Leu Leu  
45 50 55 60

aaa gca gag act ggg cgg agc gcc ctg gac gtg aag ctg aag cat gcc 362

Lys Ala Glu Thr Gly Arg Ser Ala Leu Asp Val Lys Leu Lys His Ala  
65 70 75

cgt aat caa gtg gac gtg gag atc aag cgg agg cag cgc gct gag gca 410

Arg Asn Gln Val Asp Val Glu Ile Lys Arg Arg Gln Arg Ala Glu Ala  
80 85 90

gag tgt gca aag ctg gaa caa cag att cag ctg att cga gac ata ctc 458

Glu Cys Ala Lys Leu Glu Gln Gln Ile Gln Leu Ile Arg Asp Ile Leu  
95 100 105

atg tgt gac aca tct ggc agt att cag ctg agt gag gaa caa aaa tca 506  
Met Cys Asp Thr Ser Gly Ser Ile Gln Leu Ser Glu Glu Gln Lys Ser  
110 115 120

gct ctc gct ttc ctc aac cga ggc caa gca tcc agt ggc cac gcc ggc 554  
Ala Leu Ala Phe Leu Asn Arg Gly Gln Ala Ser Ser Gly His Ala Gly  
125 130 135 140

aac aat aga ctg tca acg att gat gaa tct ggt tcc att tta tca gat 602  
Asn Asn Arg Leu Ser Thr Ile Asp Glu Ser Gly Ser Ile Leu Ser Asp  
145 150 155

atc agc ttt gac aag act gat gaa tca ctg gac tgg gat tct tct ttg 650  
Ile Ser Phe Asp Lys Thr Asp Glu Ser Leu Asp Trp Asp Ser Ser Leu  
160 165 170

gtg aag aat ttc aaa atg aag aaa cga gag aag agg cgc tcc aac agt 698  
Val Lys Asn Phe Lys Met Lys Lys Arg Glu Lys Arg Arg Ser Asn Ser  
175 180 185

aga cag ttc atc gac ggc cct cct ggg cct gtg aag aaa act tgt tcc 746  
Arg Gln Phe Ile Asp Gly Pro Pro Gly Pro Val Lys Lys Thr Cys Ser  
190 195 200

att ggc tct aca gta gac cag gca aat gaa tca ata gtt gca aaa act 794  
Ile Gly Ser Thr Val Asp Gln Ala Asn Glu Ser Ile Val Ala Lys Thr  
205 210 215 220

aca gtg act gtt ccc agt gat ggg gga ccc att gaa gct gtg tct act 842  
Thr Val Thr Val Pro Ser Asp Gly Gly Pro Ile Glu Ala Val Ser Thr  
225 230 235

att gag aca ttg ccg tcc tgg acc agg agt cgc ggg aag tca gga cct 890  
Ile Glu Thr Leu Pro Ser Trp Thr Arg Ser Arg Gly Lys Ser Gly Pro  
240 245 250

tta caa cct gtg aac agt gac tcc gct ctg aac agc agg cca ctg gag 938  
Leu Gln Pro Val Asn Ser Asp Ser Ala Leu Asn Ser Arg Pro Leu Glu  
255 260 265

cca aga act gac aca gac aat ttg ggc aca cct cag aat act gga ggc 986  
Pro Arg Thr Asp Thr Asp Asn Leu Gly Thr Pro Gln Asn Thr Gly Gly  
270 275 280

atg cgc ttg cac gac ttc gtc tca aag acg gtt att aag cct gaa tct 1034  
Met Arg Leu His Asp Phe Val Ser Lys Thr Val Ile Lys Pro Glu Ser  
285 290 295 300  
tgt gtt ccg tgt gga aag cgg atc aag ttt ggc aag ctg tct ctg aag 1082  
Cys Val Pro Cys Gly Lys Arg Ile Lys Phe Gly Lys Leu Ser Leu Lys  
305 310 315  
tgt cga gac tgt cgt ttg gtc tcc cat cca gaa tgt cgg gac cga tgt 1130  
Cys Arg Asp Cys Arg Leu Val Ser His Pro Glu Cys Arg Asp Arg Cys  
320 325 330  
ccc ctt ccc tgc atc ccc ccc ctg gtg ggg aca ccc gtt aag att gga 1178  
Pro Leu Pro Cys Ile Pro Pro Leu Val Gly Thr Pro Val Lys Ile Gly  
335 340 345  
gag ggc atg ctg gcc gac ttc gtg tcg cag gct tct ccc atg atc cct 1226  
Glu Gly Met Leu Ala Asp Phe Val Ser Gln Ala Ser Pro Met Ile Pro  
350 355 360  
gcc att gtc gtc agc tgt gtc aat gag atc gag cag cga ggc ctg act 1274  
Ala Ile Val Val Ser Cys Val Asn Glu Ile Glu Gln Arg Gly Leu Thr  
365 370 375 380  
gag gca ggc ttg tac agg atc tca ggc tgt gac cgc aca gtg aaa gaa 1322  
Glu Ala Gly Leu Tyr Arg Ile Ser Gly Cys Asp Arg Thr Val Lys Glu  
385 390 395  
ctg aaa gaa aaa ttc ctt aag gtg aaa act gtg ccc ctc ctc agc aaa 1370  
Leu Lys Glu Lys Phe Leu Lys Val Lys Thr Val Pro Leu Leu Ser Lys  
400 405 410  
gtg gac gat atc cac gtc atc tgc agc ctc ctg aag gac ttc ctg cgc 1418  
Val Asp Asp Ile His Val Ile Cys Ser Leu Leu Lys Asp Phe Leu Arg  
415 420 425  
aac ctc aaa gag ccc ctc ctg acc ttc tgg ctg agc aaa gcc ttc atg 1466  
Asn Leu Lys Glu Pro Leu Leu Thr Phe Trp Leu Ser Lys Ala Phe Met  
430 435 440  
gag gca gca gag ata aca gat gaa gac aac agc aca gcc gcc atg tac 1514  
Glu Ala Ala Glu Ile Thr Asp Glu Asp Asn Ser Thr Ala Ala Met Tyr  
445 450 455 460

cag gct gtc agt gag ctg ccc cag gcc aac agg gac acg cta gcc ttc 1562  
Gln Ala Val Ser Glu Leu Pro Gln Ala Asn Arg Asp Thr Leu Ala Phe  
465 470 475  
ctt atg atc cac cta cag aga gtg tct cag agt cca gac act aag atg 1610  
Leu Met Ile His Leu Gln Arg Val Ser Gln Ser Pro Asp Thr Lys Met  
480 485 490  
gat att gcc aat cta gct aaa gtc ttt ggc cct aca ata gtt gcc cat 1658  
Asp Ile Ala Asn Leu Ala Lys Val Phe Gly Pro Thr Ile Val Ala His  
495 500 505  
act gtg ccc aat cca gat cca gtg aca atg ttc cag gac atc aaa cgt 1706  
Thr Val Pro Asn Pro Asp Pro Val Thr Met Phe Gln Asp Ile Lys Arg  
510 515 520  
cag ctc aag gtg gtg gag cgc cta ctc tct ctc ccc ttg gag tac tgg 1754  
Gln Leu Lys Val Val Glu Arg Leu Leu Ser Leu Pro Leu Glu Tyr Trp  
525 530 535 540  
aat cag ttc atg atg gtg gag caa gag aac ata gac agc cag cga ggc 1802  
Asn Gln Phe Met Met Val Asp Gln Glu Asn Ile Asp Ser Gln Arg Gly  
545 550 555  
aat gga aac tca aca cca cgc aca cca gac gtt aaa gtg agc tta ctg 1850  
Asn Gly Asn Ser Thr Pro Arg Thr Pro Asp Val Lys Val Ser Leu Leu  
560 565 570  
ggg cct gtg acc act cct gaa ttc cag ctt gtc aag act cct tta tca 1898  
Gly Pro Val Thr Thr Pro Glu Phe Gln Leu Val Lys Thr Pro Leu Ser  
575 580 585  
agt tcc ctg tca cag agg ttg tac aac ctc tcc aag agc aca ccc aga 1946  
Ser Ser Leu Ser Gln Arg Leu Tyr Asn Leu Ser Lys Ser Thr Pro Arg  
590 595 600  
ttt ggg aac aag agc aag tct gcc acc aac tta ggt caa cag ggc aaa 1994  
Phe Gly Asn Lys Ser Lys Ser Ala Thr Asn Leu Gly Gln Gln Gly Lys  
605 610 615 620  
ttt ttc cct gct ccg tac ctc aag taa agctgtgtct gcctgtgttt 2041  
Phe Phe Pro Ala Pro Tyr Leu Lys  
625

actgcacgag acacccctgt ctgctttca gcctctgtg taatgactac ttttagcatt 2101  
ttccagactt taaataaaagt tgaacgcgta tgagagttt agtgttgcat agctccctcc 2161  
cacctggaca cttagcacct ttactagttg tcgggagctt taaaatagga gatctttacc 2221  
agggccgaag gggaaatggg tataagttgg ggctcttagg gggagggggag aggagatccc 2281  
tttggttaa agccaaatac tgctcatgaa atgactttgc tgggtgtca cttagacaat 2341  
gacagaaact gtaccttta ggtaacgtct tagttatctc aggacaggat aaagagctgc 2401  
gcagcggccc cttctcagaa cacaggcctc ttccctcccttc ggggactgac aagaagcttg 2461  
gaccctcag cgggatgggc cgggcccactg atctgaggat gcttcacttc tggctgggtt 2521  
aagctgagaa agtgcacag gctctgatct cacacagcgt gctgtttcta gccagcctct 2581  
gcctggattt tgcagtcaaa gtcaggttga tctgaagccg aattcgttct gatgcctgac 2641  
ccccttgttt gtccagtggaa gcccatttaa aaagtcagct agcagttcag aagacaattt 2701  
tcatatacgca agaaagttag ctgcttctgt ctgggtgaa gttttctgt gaaacagatc 2761  
tatatatgtt aacattggct ttttggta gcattttcca gtgttcaaaa tggtttcctt 2821  
ccctggatg ttttctgacc catactaacc cttacctgta acatgtatct ggaatattat 2881  
gtggaaaaaaaaaa taaatagctt tttcaaaatg aactttcc 2919

<210> 4  
<211> 628  
<212> PRT  
<213> Mus musculus  
<400> 4

Met	Asp	Thr	Thr	Met	Val	Asn	Leu	Trp	Thr	Leu	Phe	Glu	Gln	Leu	Val
1				5					10					15	

Arg Arg Met Glu Ile Ile Asn Glu Gly Asn Glu Ser Ile Glu Phe Ile  
20 25 30

Gln Val Val Lys Asp Phe Glu Asp Phe Arg Lys Lys Tyr Gln Arg Thr  
35 40 45

Asn Gln Glu Leu Glu Lys Phe Lys Asp Leu Leu Lys Ala Glu Thr  
50 55 60

Gly Arg Ser Ala Leu Asp Val Lys Leu Lys His Ala Arg Asn Gln Val  
65 70 75 80

Asp Val Glu Ile Lys Arg Arg Gln Arg Ala Glu Ala Glu Cys Ala Lys  
85 90 95

Leu Glu Gln Gln Ile Gln Leu Ile Arg Asp Ile Leu Met Cys Asp Thr  
100 105 110

Ser Gly Ser Ile Gln Leu Ser Glu Glu Gln Lys Ser Ala Leu Ala Phe  
115 120 125

Leu Asn Arg Gly Gln Ala Ser Ser Gly His Ala Gly Asn Asn Arg Leu  
130 135 140

Ser Thr Ile Asp Glu Ser Gly Ser Ile Leu Ser Asp Ile Ser Phe Asp  
145 150 155 160

Lys Thr Asp Glu Ser Leu Asp Trp Asp Ser Ser Leu Val Lys Asn Phe  
165 170 175

Lys Met Lys Lys Arg Glu Lys Arg Arg Ser Asn Ser Arg Gln Phe Ile  
180 185 190

Asp Gly Pro Pro Gly Pro Val Lys Lys Thr Cys Ser Ile Gly Ser Thr  
195 200 205

Val Asp Gln Ala Asn Glu Ser Ile Val Ala Lys Thr Thr Val Thr Val  
210 215 220

Pro Ser Asp Gly Gly Pro Ile Glu Ala Val Ser Thr Ile Glu Thr Leu  
225 230 235 240

Pro Ser Trp Thr Arg Ser Arg Gly Lys Ser Gly Pro Leu Gln Pro Val  
245 250 255

Asn Ser Asp Ser Ala Leu Asn Ser Arg Pro Leu Glu Pro Arg Thr Asp  
260 265 270

Thr Asp Asn Leu Gly Thr Pro Gln Asn Thr Gly Gly Met Arg Leu His  
275 280 285

Asp Phe Val Ser Lys Thr Val Ile Lys Pro Glu Ser Cys Val Pro Cys  
290 295 300

Gly Lys Arg Ile Lys Phe Gly Lys Leu Ser Leu Lys Cys Arg Asp Cys  
305 310 315 320

Arg Leu Val Ser His Pro Glu Cys Arg Asp Arg Cys Pro Leu Pro Cys  
325 330 335

Ile Pro Pro Leu Val Gly Thr Pro Val Lys Ile Gly Glu Gly Met Leu  
340 345 350

Ala Asp Phe Val Ser Gln Ala Ser Pro Met Ile Pro Ala Ile Val Val  
355 360 365

Ser Cys Val Asn Glu Ile Glu Gln Arg Gly Leu Thr Glu Ala Gly Leu  
370 375 380

Tyr Arg Ile Ser Gly Cys Asp Arg Thr Val Lys Glu Leu Lys Glu Lys  
385 390 395 400

Phe Leu Lys Val Lys Thr Val Pro Leu Leu Ser Lys Val Asp Asp Ile  
405 410 415

His Val Ile Cys Ser Leu Leu Lys Asp Phe Leu Arg Asn Leu Lys Glu  
420 425 430

Pro Leu Leu Thr Phe Trp Leu Ser Lys Ala Phe Met Glu Ala Ala Glu  
435 440 445

Ile Thr Asp Glu Asp Asn Ser Thr Ala Ala Met Tyr Gln Ala Val Ser  
450 455 460

Glu Leu Pro Gln Ala Asn Arg Asp Thr Leu Ala Phe Leu Met Ile His  
465 470 475 480

Leu Gln Arg Val Ser Gln Ser Pro Asp Thr Lys Met Asp Ile Ala Asn  
485 490 495

Leu Ala Lys Val Phe Gly Pro Thr Ile Val Ala His Thr Val Pro Asn  
500 505 510

Pro Asp Pro Val Thr Met Phe Gln Asp Ile Lys Arg Gln Leu Lys Val  
515 520 525

Val Glu Arg Leu Leu Ser Leu Pro Leu Glu Tyr Trp Asn Gln Phe Met  
530 535 540

Met Val Asp Gln Glu Asn Ile Asp Ser Gln Arg Gly Asn Gly Asn Ser  
545 550 555 560

Thr Pro Arg Thr Pro Asp Val Lys Val Ser Leu Leu Gly Pro Val Thr  
565 570 575

Thr Pro Glu Phe Gln Leu Val Lys Thr Pro Leu Ser Ser Ser Leu Ser  
580 585 590

Gln Arg Leu Tyr Asn Leu Ser Lys Ser Thr Pro Arg Phe Gly Asn Lys

595

600

605

Ser Lys Ser Ala Thr Asn Leu Gly Gln Gln Gly Lys Phe Phe Pro Ala  
610 615 620

Pro Tyr Leu Lys  
625

<210> 5  
<211> 2046  
<212> DNA  
<213> Caenorhabditis elegans

<220>  
<221> CDS  
<222> (1)..(2046)

400 > 5

atg aag tcc agt aca tca aaa gag aag gtg tgc ggc gaa aac tcg cgt 48

Met Lys Ser Ser Thr Ser Lys Glu Lys Val Cys Gly Glu Asn Ser Arg  
1 5 10 15

cac att ttc aac atg att cta aac tca cag cga ccg caa ttc gat att 96

His Ile Phe Asn Met Ile Leu Asn Ser Gln Arg Pro Gln Phe Asp Ile  
20 25 30

aag gat ata gga atg ttt cat ttg att gat gag att gag cgt ctc cgc 144

Lys Asp Ile Gly Met Phe His Leu Ile Asp Glu Ile Glu Arg Leu Arg  
35 40 45

aag ctg tgg aaa gat tcc gag gaa tcc aaa aag cgg ctg aat gca gat 192

Lys Leu Trp Lys Asp Ser Glu Glu Ser Lys Lys Arg Leu Asn Ala Asp  
50 55 60

atg aga gag gcc gaa gaa gca ctt gca aaa gct cgc aag aag ctg gca 240

Met Arg Glu Ala Glu Glu Ala Leu Ala Lys Ala Arg Lys Lys Leu Ala  
65 70 75 80

atg ttc gat atc gat gtc aaa gac act cag aaa cat tta cgc gcg ttg 288

Met Phe Asp Ile Asp Val Lys Asp Thr Gln Lys His Leu Arg Ala Leu  
85 90 95

atg gaa gaa aat aag gcg ttg aag ctc gat cta aac gtc tac gag act 336

Met Glu Glu Asn Lys Ala Leu Lys Leu Asp Leu Asn Val Tyr Glu Thr  
100 105 110

cgtaaagcagctgaaa gatgcgtatc aag aac ggtata ttc aat agt 384  
Arg Glu Lys Gln Leu Lys Asp Ala Met Lys Asn Gly Ile Phe Asn Ser  
115 120 125

ctcacc aag gaa gac cgc gat cag ttc aag ttt ctt cac gag cca ctg 432  
Leu Thr Lys Glu Asp Arg Asp Gln Phe Lys Phe Leu His Glu Pro Leu  
130 135 140

gtccgg aca tac tcg aaa cgg gtg cag cag agg cat cca cat ttg atg 480  
Val Arg Thr Tyr Ser Lys Arg Val Gln Gln Arg His Pro His Leu Met  
145 150 155 160

gag gac aca cag gac gat gag gac gat agt gag gtg gat tac gat gaa 528  
Glu Asp Thr Gln Asp Asp Glu Asp Asp Ser Glu Val Asp Tyr Asp Glu  
165 170 175

act gga gac agt ttc gag gaa gtt att cat ttg cgc aat gga aga gag 576  
Thr Gly Asp Ser Phe Glu Glu Val Ile His Leu Arg Asn Gly Arg Glu  
180 185 190

gtcagaaga agc tca gct gct gga aac gca gtt ggt ggc aag cgg aga 624  
Val Arg Arg Ser Ser Ala Ala Gly Asn Ala Val Gly Gly Lys Arg Arg  
195 200 205

agc gcg tca gca cat gcg att act gct gct gcc aat tcg aag agg agc 672  
Ser Ala Ser Ala His Ala Ile Thr Ala Ala Ala Asn Ser Lys Arg Ser  
210 215 220

aga agc cgt gtt atg aca gct act ata gat gaa gag ccg aat gag ggt 720  
Arg Ser Arg Val Met Thr Ala Thr Ile Asp Glu Glu Pro Asn Glu Gly  
225 230 235 240

ggtaaca cct cca aaa aga tgc cgt gat gat ggt tct aca cct cat caa 768  
Gly Thr Pro Pro Lys Arg Cys Arg Asp Asp Gly Ser Thr Pro His Gln  
245 250 255

gaa atg aca act acc acc act acc acc acc act act att cat aac 816  
Glu Met Thr Thr Thr Thr Thr Thr Thr Thr Ile His Asn  
260 265 270

tct cga gct cag aac cag gac cgc cca cgt gtc tca ctt cac cgc cag 864  
Ser Arg Ala Gln Asn Gln Asp Pro Pro Arg Val Ser Leu His Arg Gln  
275 280 285

ctc acc cgc agg agc ttg agc tgt gga agt att cca tca tgc gat caa 912  
Leu Thr Arg Arg Ser Leu Ser Cys Gly Ser Ile Pro Ser Cys Asp Gln  
290 295 300  
aca cca gga caa acc aca aat aac atc ggc ctc ggc atg tcg tcc gcc 960  
Thr Pro Gly Gln Thr Thr Asn Asn Ile Gly Leu Gly Met Ser Ser Ala  
305 310 315 320  
att ctc acc aaa agc aca ctt gat atc cga acc ctg aaa cgt ggc acg 1008  
Ile Leu Thr Lys Ser Thr Leu Asp Ile Arg Thr Leu Lys Arg Gly Thr  
325 330 335  
ccg gcg tgg act aat gga aca act cgt gac atc gca atg aga cca cac 1056  
Pro Ala Trp Thr Asn Gly Thr Thr Arg Asp Ile Ala Met Arg Pro His  
340 345 350  
acg ttt ata gag gca gga atc aaa gcg atg cga aaa tgc gac aaa tgt 1104  
Thr Phe Ile Glu Ala Gly Ile Lys Ala Met Arg Lys Cys Asp Lys Cys  
355 360 365  
gct aca gcc ctg aag ctc gcc aca tca atg aaa tgc aga gac tgt cac 1152  
Ala Thr Ala Leu Lys Leu Ala Thr Ser Met Lys Cys Arg Asp Cys His  
370 375 380  
cag gtt gtc cat cgt agt tgc tgc aac aaa ctt cat ctc ccg tgc ata 1200  
Gln Val Val His Arg Ser Cys Cys Asn Lys Leu His Leu Pro Cys Ile  
385 390 395 400  
cca cgc ccc aag acg atg atg acg ccc aaa tcc gca tta cgt gga gcc 1248  
Pro Arg Pro Lys Thr Met Met Thr Pro Lys Ser Ala Leu Arg Gly Ala  
405 410 415  
aag ccg ggc gca gga gag ttc cga ctt caa gat ttg tgc aca tct cgc 1296  
Lys Pro Gly Ala Gly Glu Phe Arg Leu Gln Asp Leu Cys Thr Ser Ala  
420 425 430  
aag cca atg atc ccg gca gca gtt att cat tgt gtg gtt gcc ctg gag 1344  
Lys Pro Met Ile Pro Ala Ala Val Ile His Cys Val Val Ala Leu Glu  
435 440 445  
gct cgt gga ctc acg cag gaa ggt att tac cgc gtt cct ggg cag gtt 1392  
Ala Arg Gly Leu Thr Gln Glu Gly Ile Tyr Arg Val Pro Gly Gln Val  
450 455 460

aga act gtc aat gtg ctt ttg gac gag ttg aga tca aaa acg gta ccc 1440  
Arg Thr Val Asn Val Leu Leu Asp Glu Leu Arg Ser Lys Thr Val Pro  
465 470 475 480  
aac gtg ggc ctt cac gac gtt gag gtc atc aca gac acc ttg aaa cgg 1488  
Asn Val Gly Leu His Asp Val Glu Val Ile Thr Asp Thr Leu Lys Arg  
485 490 495  
ttc cta aga gat ctt aaa gac ccg ttg atc cca aga acg tct cgt caa 1536  
Phe Leu Arg Asp Leu Lys Asp Pro Leu Ile Pro Arg Thr Ser Arg Gln  
500 505 510  
gag ctc atc gtt gct gca aac ctc tac tct acg gat cca gat aat gga 1584  
Glu Leu Ile Val Ala Ala Asn Leu Tyr Ser Thr Asp Pro Asp Asn Gly  
515 520 525  
cgt ctc gcc ctg aat cga gtg atc tgt gag ctc ccc caa gcg aat cga 1632  
Arg Leu Ala Leu Asn Arg Val Ile Cys Glu Leu Pro Gln Ala Asn Arg  
530 535 540  
gac acc ctc gcc tac ctt ttc att cac tgg cgc aaa gtt atc gca caa 1680  
Asp Thr Leu Ala Tyr Leu Phe Ile His Trp Arg Lys Val Ile Ala Gln  
545 550 555 560  
tcg agt cgc aac aag atg aac tgc gaa gcg atg gcg cgg atg gtg gct 1728  
Ser Ser Arg Asn Lys Met Asn Cys Glu Ala Met Ala Arg Met Val Ala  
565 570 575  
ccg gcg gtg atg ggt cat cca gtg aag caa tcg cag tcc caa gcg ata 1776  
Pro Ala Val Met Gly His Pro Val Lys Gln Ser Gln Ser Gln Ala Ile  
580 585 590  
gct ggc aga gat gcc acg gat tgc cat cga gcg atg act gct cta ttt 1824  
Ala Gly Arg Asp Ala Thr Asp Cys His Arg Ala Met Thr Ala Leu Phe  
595 600 605  
gaa ttt gat gat gta tat tgg caa cga ttc cta ggg aca tct gca gtt 1872  
Glu Phe Asp Asp Val Tyr Trp Gln Arg Phe Leu Gly Thr Ser Ala Val  
610 615 620  
tcc atg gct tct aat caa att gaa acg gct cga cat cag gac aat ttt 1920  
Ser Met Ala Ser Asn Gln Ile Glu Thr Ala Arg His Gln Asp Asn Phe  
625 630 635 640

gct ctc tgt gat cgt agc atc ctt gga cca gtt aca aca tca cca gcc 1968  
Ala Leu Cys Asp Arg Ser Ile Leu Gly Pro Val Thr Thr Ser Pro Ala  
645 650 655  
act ccc ctg ctt gct cggt gcc aac gcg act cga gca cgt ggt gct 2016  
Thr Pro Leu Leu Ala Arg Ser Ala Asn Ala Thr Arg Ala Arg Gly Ala  
660 665 670  
cat ctg ctg ggg tcg atg ttc cac gat tag 2046  
His Leu Leu Gly Ser Met Phe His Asp  
675 680

<210> 6  
<211> 681  
<212> PRT  
<213> Caenorhabditis elegans  
  
<400> 6

Met Lys Ser Ser Thr Ser Lys Glu Lys Val Cys Gly Glu Asn Ser Arg  
1 5 10 15  
His Ile Phe Asn Met Ile Leu Asn Ser Gln Arg Pro Gln Phe Asp Ile  
20 25 30  
Lys Asp Ile Gly Met Phe His Leu Ile Asp Glu Ile Glu Arg Leu Arg  
35 40 45  
Lys Leu Trp Lys Asp Ser Glu Glu Ser Lys Lys Arg Leu Asn Ala Asp  
50 55 60  
Met Arg Glu Ala Glu Glu Ala Leu Ala Lys Ala Arg Lys Lys Leu Ala  
65 70 75 80  
Met Phe Asp Ile Asp Val Lys Asp Thr Gln Lys His Leu Arg Ala Leu  
85 90 95  
Met Glu Glu Asn Lys Ala Leu Lys Leu Asp Leu Asn Val Tyr Glu Thr  
100 105 110  
Arg Glu Lys Gln Leu Lys Asp Ala Met Lys Asn Gly Ile Phe Asn Ser  
115 120 125  
Leu Thr Lys Glu Asp Arg Asp Gln Phe Lys Phe Leu His Glu Pro Leu  
130 135 140  
Val Arg Thr Tyr Ser Lys Arg Val Gln Gln Arg His Pro His Leu Met  
145 150 155 160  
Glu Asp Thr Gln Asp Asp Glu Asp Asp Ser Glu Val Asp Tyr Asp Glu  
165 170 175

Thr Gly Asp Ser Phe Glu Glu Val Ile His Leu Arg Asn Gly Arg Glu  
180 185 190

Val Arg Arg Ser Ser Ala Ala Gly Asn Ala Val Gly Gly Lys Arg Arg  
195 200 205

Ser Ala Ser Ala His Ala Ile Thr Ala Ala Ala Asn Ser Lys Arg Ser  
210 215 220

Arg Ser Arg Val Met Thr Ala Thr Ile Asp Glu Glu Pro Asn Glu Gly  
225 230 235 240

Gly Thr Pro Pro Lys Arg Cys Arg Asp Asp Gly Ser Thr Pro His Gln  
245 250 255

Glu Met Thr Thr Thr Thr Thr Thr Thr Thr Thr Ile His Asn  
260 265 270

Ser Arg Ala Gln Asn Gln Asp Pro Pro Arg Val Ser Leu His Arg Gln  
275 280 285

Leu Thr Arg Arg Ser Leu Ser Cys Gly Ser Ile Pro Ser Cys Asp Gln  
290 295 300

Thr Pro Gly Gln Thr Thr Asn Asn Ile Gly Leu Gly Met Ser Ser Ala  
305 310 315 320

Ile Leu Thr Lys Ser Thr Leu Asp Ile Arg Thr Leu Lys Arg Gly Thr  
325 330 335

Pro Ala Trp Thr Asn Gly Thr Thr Arg Asp Ile Ala Met Arg Pro His  
340 345 350

Thr Phe Ile Glu Ala Gly Ile Lys Ala Met Arg Lys Cys Asp Lys Cys  
355 360 365

Ala Thr Ala Leu Lys Leu Ala Thr Ser Met Lys Cys Arg Asp Cys His  
370 375 380

Gln Val Val His Arg Ser Cys Cys Asn Lys Leu His Leu Pro Cys Ile  
385 390 395 400

Pro Arg Pro Lys Thr Met Met Thr Pro Lys Ser Ala Leu Arg Gly Ala  
405 410 415

Lys Pro Gly Ala Gly Glu Phe Arg Leu Gln Asp Leu Cys Thr Ser Ala  
420 425 430

Lys Pro Met Ile Pro Ala Ala Val Ile His Cys Val Val Ala Leu Glu  
435 440 445

Ala Arg Gly Leu Thr Gln Glu Gly Ile Tyr Arg Val Pro Gly Gln Val  
450 455 460

Arg Thr Val Asn Val Leu Leu Asp Glu Leu Arg Ser Lys Thr Val Pro

465	470	475	480
Asn Val Gly Leu His Asp Val Glu Val Ile Thr Asp Thr Leu Lys Arg			
485	490	495	
Phe Leu Arg Asp Leu Lys Asp Pro Leu Ile Pro Arg Thr Ser Arg Gln			
500	505	510	
Glu Leu Ile Val Ala Ala Asn Leu Tyr Ser Thr Asp Pro Asp Asn Gly			
515	520	525	
Arg Leu Ala Leu Asn Arg Val Ile Cys Glu Leu Pro Gln Ala Asn Arg			
530	535	540	
Asp Thr Leu Ala Tyr Leu Phe Ile His Trp Arg Lys Val Ile Ala Gln			
545	550	555	560
Ser Ser Arg Asn Lys Met Asn Cys Glu Ala Met Ala Arg Met Val Ala			
565	570	575	
Pro Ala Val Met Gly His Pro Val Lys Gln Ser Gln Ser Gln Ala Ile			
580	585	590	
Ala Gly Arg Asp Ala Thr Asp Cys His Arg Ala Met Thr Ala Leu Phe			
595	600	605	
Glu Phe Asp Asp Val Tyr Trp Gln Arg Phe Leu Gly Thr Ser Ala Val			
610	615	620	
Ser Met Ala Ser Asn Gln Ile Glu Thr Ala Arg His Gln Asp Asn Phe			
625	630	635	640
Ala Leu Cys Asp Arg Ser Ile Leu Gly Pro Val Thr Thr Ser Pro Ala			
645	650	655	
Thr Pro Leu Leu Ala Arg Ser Ala Asn Ala Thr Arg Ala Arg Gly Ala			
660	665	670	
His Leu Leu Gly Ser Met Phe His Asp			
675	680		